

SEQUENCE LISTING

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<120> REGULATOR OF NOTCH SIGNALING ACTIVITY

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<151> 1998-11-03

<160> 16

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<210> 1

<211> 480

<212> PRT

<213> Drosophila sp.

<400> 1

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Ala	Arg	Leu	Val	Tyr	Thr	Gly	Glu	Glu	Ala	Gly	Pro	Pro	Ile	Asp	Leu
			20					25					30		
Pro	Ala	Gly	Ile	Thr	Thr	Gln	Gln	Leu	Gly	Leu	Ile	Cys	Asn	Ala	Leu
		35					40					45			
Leu	Lys	Asn	Glu	Glu	Ala	Thr	Pro	Tyr	Leu	Phe	Phe	Val	Gly	Glu	Asp
	50					55					60				
Glu	Ile	Lys	Lys	Ser	Leu	Glu	Asp	Thr	Leu	Asp	Leu	Ala	Ser	Val	Asp
65					70					75					80
Thr	Glu	Asn	Val	Ile	Asp	Ile	Val	Tyr	Gln	Pro	Gln	Ala	Val	Phe	Lys
				85					90					95	
Val	Arg	Pro	Val	Thr	Arg	Cys	Thr	Ser	Ser	Met	Pro	Gly	His	Ala	Glu
			100					105					110		
Ala	Val	Val	Ser	Leu	Asn	Phe	Ser	Pro	Asp	Gly	Ala	His	Leu	Ala	Ser
		115					120					125			
Gly	Ser	Gly	Asp	Thr	Thr	Val	Arg	Leu	Trp	Asp	Leu	Asn	Thr	Glu	Thr
		130				135					140				

Pro His Phe Thr Cys Thr Gly His Lys Gln Trp Val Leu Cys Val Ser
 145 150 155 160
 Trp Ala Pro Asp Gly Lys Arg Leu Ala Ser Gly Cys Lys Ala Gly Ser
 165 170 175
 Ile Ile Ile Trp Asp Pro Glu Thr Gly Gln Gln Lys Gly Arg Pro Leu
 180 185 190
 Ser Gly His Lys Lys His Ile Asn Cys Leu Ala Trp Glu Pro Tyr His
 195 200 205
 Arg Asp Pro Glu Cys Arg Lys Leu Ala Ser Ala Ser Gly Asp Gly Asp
 210 215 220
 Cys Arg Ile Trp Asp Val Lys Leu Gly Gln Cys Leu Met Asn Ile Ala
 225 230 235 240
 Gly His Thr Asn Ala Val Thr Ala Val Arg Trp Gly Gly Ala Gly Leu
 245 250 255
 Ile Tyr Thr Ser Ser Lys Asp Arg Thr Val Lys Met Trp Arg Ala Ala
 260 265 270
 Asp Gly Ile Leu Cys Arg Thr Phe Ser Gly His Ala His Trp Val Asn
 275 280 285
 Asn Ile Ala Leu Ser Thr Asp Tyr Val Leu Arg Thr Gly Pro Phe His
 290 295 300
 Pro Val Lys Asp Arg Ser Lys Ser His Leu Ser Leu Ser Thr Glu Glu
 305 310 315 320
 Leu Gln Glu Ser Ala Leu Lys Arg Tyr Gln Ala Val Cys Pro Asp Glu
 325 330 335
 Val Glu Ser Leu Val Ser Cys Ser Asp Asp Asn Thr Leu Tyr Leu Trp
 340 345 350
 Arg Asn Asn Gln Asn Lys Cys Val Glu Arg Met Thr Gly His Gln Asn
 355 360 365
 Val Val Asn Asp Val Lys Tyr Ser Pro Asp Val Lys Leu Ile Ala Ser
 370 375 380
 Ala Ser Phe Asp Lys Ser Val Arg Leu Trp Arg Ala Ser Asp Gly Gln
 385 390 395 400
 Tyr Met Ala Thr Phe Arg Gly His Val Gln Ala Val Tyr Thr Val Ala
 405 410 415
 Trp Ser Ala Asp Ser Arg Leu Ile Val Ser Gly Ser Lys Asp Ser Thr
 420 425 430
 Leu Lys Val Trp Ser Val Gln Thr Lys Lys Leu Ala Gln Glu Leu Pro
 435 440 445

Gly His Ala Asp Glu Val Phe Gly Val Asp Trp Ala Pro Asp Gly Ser
 450 455 460

Arg Val Ala Ser Gly Gly Lys Asp Lys Val Ile Lys Leu Trp Ala Tyr
 465 470 475 480

<210> 2
 <211> 1555
 <212> DNA
 <213> *Drosophila* sp.

<400> 2
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 actaccacgc aattgggact gatttgcaac gcgctgctga aaaacgagga agccactcca 180
 tatttgtttt tcgtgggcga ggatgagatc aagaagagcc tggaggacac gttggacttg 240
 gcgtcagtg acaccgaaa cgtgatcgat attgtgtatc agccacaggc ggttttcaaa 300
 gtgcgcccag tgacaagatg cacgagttcc atgccgggac acgccgaggc tgtggtttcg 360
 ctgaatttca gcccggatgg tgetcatctc gccagtggaa gtggcgacac cacagtgcga 420
 ttgtgggatc ttaacacaga gacaccgcac ttcacctgca caggtcataa gcagtgggtt 480
 ctgtgcgtat cctgggctcc ggatggcaaa cggttgcca gcggttgcaa agcgggctct 540
 ataatcatct gggacccgga gacgggtcag cagaaggggc gacccttgag tgggcacaag 600
 aaacacatca actgcctcgc ctgggaaccg tatcatcgcg atccggagtg caggaaactt 660
 gcttccgcca gtggagacgg ggactgccgg atttgggacg taaaattggg ccagtgcctt 720
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 aacaagtgcg ttgagcgcac gacagggcac cagaacgtgg tcaacgatgt gaaatattcg 1140
 ccggatgtaa agctaattgc gtctgcttca tttgacaagt cagtgcgtct gtggcgagcc 1200
 agcgatggtc agtacatggc caccttccgg ggtcatgtgc aggcgtgtta cacggttgcc 1260
 tggtcgcgag actcccgtt gattgtttcc ggcagcaaag actcaactct aaaagtatgg 1320
 agtgtgcaga cgaagaaact ggcacaggag ctgcctggac atgcggatga ggtgttcgga 1380
 gtggactggg cgcccgatgg ctctagagtt gcctctggtg gcaaggacaa agttataaag 1440
 ctatgggctt attaacaaat cattaacttg tacacggtaa gaaaataactt aggaataaag 1500
 taaaacgtcc tgagtaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1555

<210> 3
 <211> 513
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 3
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 1 5 10 15
 Gln Leu Pro Arg Glu Val Ala Ile Ile Pro Lys Asp Leu Pro Asn Val
 20 25 30
 Ser Ile Lys Phe Gln Ala Leu Asp Thr Gly Asp Asn Val Gly Gly Ala
 35 40 45

Leu Arg Val Pro Gly Ala Ile Ser Glu Lys Gln Leu Glu Glu Leu Leu
 50 55 60
 Asn Gln Leu Asn Gly Thr Ser Asp Asp Pro Val Pro Tyr Thr Phe Ser
 65 70 75 80
 Cys Thr Ile Gln Gly Lys Lys Ala Ser Asp Pro Val Lys Thr Ile Asp
 85 90 95
 Ile Thr Asp Asn Leu Tyr Ser Ser Leu Ile Lys Pro Gly Tyr Asn Ser
 100 105 110
 Thr Glu Asp Gln Ile Thr Leu Leu Tyr Thr Pro Arg Ala Val Phe Lys
 115 120 125
 Val Lys Pro Val Thr Arg Ser Ser Ser Ala Ile Ala Gly His Gly Ser
 130 135 140
 Thr Ile Leu Cys Ser Ala Phe Ala Pro His Thr Ser Ser Arg Met Val
 145 150 155 160
 Thr Gly Ala Gly Asp Asn Thr Ala Arg Ile Trp Asp Cys Asp Thr Gln
 165 170 175
 Thr Pro Met His Thr Leu Lys Gly His Tyr Asn Trp Val Leu Cys Val
 180 185 190
 Ser Trp Ser Pro Asp Gly Glu Val Ile Ala Thr Gly Ser Met Asp Asn
 195 200 205
 Thr Ile Arg Leu Trp Asp Pro Lys Ser Gly Gln Cys Leu Gly Asp Ala
 210 215 220
 Leu Arg Gly His Ser Lys Trp Ile Thr Ser Leu Ser Trp Glu Pro Ile
 225 230 235 240
 Leu Val Lys Pro Gly Ser Lys Pro Arg Leu Ala Ser Ser Ser Lys Asp
 245 250 255
 Gly Thr Ile Lys Ile Trp Asp Thr Val Ser Arg Val Cys Gln Tyr Thr
 260 265 270
 Met Ser Gly His Thr Asn Ser Val Ser Cys Val Lys Trp Gly Gly Gln
 275 280 285
 Gly Leu Leu Tyr Ser Gly Ser His Asp Arg Thr Val Arg Val Trp Asp
 290 295 300
 Ile Asn Ser Gln Gly Arg Cys Ile Asn Ile Leu Lys Ser His Ala His
 305 310 315 320
 Trp Val Asn His Leu Ser Leu Ser Thr Asp Tyr Ala Leu Arg Ile Gly
 325 330 335
 Ala Phe Asp His Thr Gly Lys Lys Pro Ser Thr Pro Glu Glu Ala Gln
 340 345 350

Lys Lys Ala Leu Glu Asn Tyr Glu Lys Ile Cys Lys Lys Asn Gly Asn
 355 360 365
 Ser Glu Glu Met Met Val Thr Ala Ser Asp Asp Tyr Thr Met Phe Leu
 370 375 380
 Trp Asn Pro Leu Lys Ser Thr Lys Pro Ile Ala Arg Met Thr Gly His
 385 390 395 400
 Gln Lys Leu Val Asn His Val Ala Phe Ser Pro Asp Gly Arg Tyr Ile
 405 410 415
 Val Ser Ala Ser Phe Asp Asn Ser Ile Lys Leu Trp Asp Gly Arg Asp
 420 425 430
 Gly Lys Phe Ile Ser Thr Phe Arg Gly His Ile Ala Ser Val Tyr Gln
 435 440 445
 Val Ala Trp Ser Ser Asp Cys Arg Leu Leu Val Ser Cys Ser Lys Asp
 450 455 460
 Thr Thr Leu Lys Val Trp Asp Val Arg Thr Arg Lys Leu Ser Val Asp
 465 470 475 480
 Leu Pro Gly Ile Lys Thr Lys Leu Tyr Val Asp Trp Ser Val Asp Gly
 485 490 495
 Lys Arg Val Cys Ser Gly Gly Lys Asp Lys Met Val Arg Leu Trp Thr
 500 505 510

His

<210> 4
 <211> 351
 <212> PRT
 <213> Codonanthus elegans

<220>
 <221> MOD_RES
 <222> (184)..(185)
 <223> Variable amino acid

<400> 4
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 1 5 10 15
 Ile Leu Val Pro Val Asp Ile Ser Thr Asn Glu Leu Gln Ile Leu Cys
 20 25 30
 Asn Gln Leu Leu Gly Ser Arg Phe Cys Leu Asn Asn Glu Phe Ser Val
 35 40 45
 Ser Gly Ala Glu Ile Val Asp Ser Ile Arg Lys Ser Leu Glu Glu Ile
 50 55 60

Asp Phe Glu Thr Leu Lys Leu Val Tyr Gln Pro Gln Ala Val Phe Arg
 65 70 75 80
 Val Arg Pro Val Thr Arg Cys Ser Ala Ser Ile Pro Gly His Gly Glu
 85 90 95
 Pro Val Ile Ser Ala Gln Phe Ser Pro Asp Gly Arg Gly Leu Ala Ser
 100 105 110
 Gly Ser Gly Asp Gln Thr Met Arg Ile Trp Asp Ile Glu Leu Glu Leu
 115 120 125
 Pro Leu His Thr Cys Lys Ser His Lys Ser Trp Val Leu Cys Ile Ala
 130 135 140
 Trp Ser Pro Asp Ala Thr Lys Ile Ala Ser Ala Cys Lys Asn Gly Glu
 145 150 155 160
 Ile Cys Ile Trp Asn Ala Lys Thr Gly Glu Gln Ile Gly Lys Thr Leu
 165 170 175
 Lys Arg His Lys Gln Trp Ile Xaa Xaa Leu Ala Trp Gln Pro Thr Val
 180 185 190
 Lys Met Trp Arg Ala Asp Asp Gly Val Met Cys Arg Asn Met Thr Gly
 195 200 205
 His Ala His Trp Ile Asn Thr Leu Ala Leu Asn Thr Asp Tyr Ala Leu
 210 215 220
 Arg Thr Ser Cys Phe Glu Pro Ser Lys Ile Asn Arg Met Thr Gly His
 225 230 235 240
 Met Gln Leu Val Asn Gln Val Val Phe Ser Pro Asp Thr Arg Tyr Ala
 245 250 255
 Ser Ala Ser Phe Asp Lys Ser Val Lys Leu Trp Cys Gly Arg Thr Gly
 260 265 270
 Lys Tyr Leu Ala Ser Phe Arg Gly His Val Gly Pro Val Tyr Gln Val
 275 280 285
 Ala Trp Ser Ala Asp Ser Arg Leu Leu Val Ser Gly Ser Ala Asp Ser
 290 295 300
 Thr Leu Lys Val Phe Glu Leu Lys Thr Lys Ser Leu Tyr Tyr Asp Leu
 305 310 315 320
 Pro Gly His Gly Asp Glu Val Phe Thr Val Asp Trp Ser Pro Glu Gly
 325 330 335
 Thr Lys Val Val Ser Gly Gly Lys Asp Lys Val Leu Lys Leu Trp
 340 345 350

<210> 5

<211> 103

<212> PRT
 <213> Mus sp.

<220>
 <221> MOD_RES
 <222> (39)
 <223> Variable amino acid

<400> 5
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 1 5 10 15
 Asp Glu Gly Gly Gln Leu Leu Gly Ser Pro Phe Asp Val Pro Val Asp
 20 25 30
 Ile Thr Pro Asp Lys Leu Xaa Leu Val Cys Asn Ala Leu Leu Ala Gln
 35 40 45
 Glu Glu Pro Leu Pro Leu Ala Phe Tyr Val His Asp Ala Glu Ile Val
 50 55 60
 Ser Ser Leu Gly Lys Thr Leu Glu Ser Gln Ser Val Glu Thr Glu Lys
 65 70 75 80
 Ile Val Asp Ile Ile Tyr Gln Pro Gln Ala Val Phe Arg Val Arg Ala
 85 90 95
 Val Thr Arg Cys Thr Ser Ser
 100

<210> 6
 <211> 78
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (66)
 <223> Variable amino acid

<400> 6
 Gly Ser Pro Phe Asp Val Pro Val Asp Ile Thr Pro Asp Arg Leu Gln
 1 5 10 15
 Leu Val Cys Asn Ala Leu Leu Ala Gln Glu Asp Pro Cys Pro Leu Ala
 20 25 30
 Phe Phe Val His Asp Ala Glu Ile Val Ser Ser Leu Gly Lys Thr Leu
 35 40 45
 Glu Ser Gln Ala Val Glu Thr Glu Lys Val Leu Asp Ile Tyr Gln Pro
 50 55 60
 Gln Xaa Leu Phe Arg Val Arg Ala Val Thr Arg Cys Thr Ser
 65 70 75

<210> 7
 <211> 476
 <212> PRT
 <213> *Xenopus laevis*

<400> 7

Met	Lys	Glu	Asp	Val	Gly	Arg	Leu	Leu	Ile	Gln	Phe	Lys	Asn	Glu	Asn	1	5	10	15
Gly	Glu	Gly	Leu	Gly	Thr	Pro	Phe	Asp	Val	Pro	Leu	Asp	Ile	Thr	Pro	20	25	30	
Asp	Lys	Leu	Gln	Leu	Val	Cys	Asn	Ala	Leu	Leu	Gln	Glu	Glu	Asp	Pro	35	40	45	
Val	Pro	Leu	Ala	Phe	Phe	Val	Gln	Asp	Leu	Glu	Ile	Val	Thr	Ser	Leu	50	55	60	
Asp	Lys	Thr	Leu	Glu	Lys	Gln	Ser	Val	Glu	Thr	Glu	Lys	Val	Ile	Asp	65	70	75	80
Ile	Ile	Tyr	Gln	Pro	Gln	Ala	Val	Phe	Lys	Val	Arg	Ala	Val	Thr	Arg	85	90	95	
Cys	Thr	Ser	Ser	Leu	Glu	Gly	His	Thr	Glu	Ala	Val	Ile	Ser	Val	Ala	100	105	110	
Phe	Ser	Pro	Thr	Gly	Lys	Tyr	Leu	Ala	Ser	Gly	Ser	Gly	Asp	Thr	Thr	115	120	125	
Val	Arg	Phe	Trp	Asp	Leu	Ser	Thr	Glu	Thr	Pro	His	Phe	Thr	Ser	Lys	130	135	140	
Gly	His	Thr	His	Trp	Val	Leu	Ser	Ile	Ala	Trp	Ser	Pro	Asp	Gly	Lys	145	150	155	160
Lys	Leu	Ala	Ser	Gly	Cys	Lys	Asn	Ser	Gln	Ile	Phe	Ile	Trp	Asp	Pro	165	170	175	
Ser	Thr	Gly	Lys	Gln	Ile	Gly	Lys	Pro	Leu	Thr	Gly	His	Ser	Lys	Trp	180	185	190	
Ile	Thr	Trp	Leu	Cys	Trp	Glu	Pro	Leu	His	Leu	Asn	Pro	Glu	Ser	Arg	195	200	205	
Tyr	Leu	Ala	Ser	Ala	Ser	Lys	Asp	Cys	Thr	Ile	Arg	Ile	Trp	Asp	Thr	210	215	220	
Val	Met	Gly	Gln	Cys	Gln	Lys	Ile	Leu	Thr	Ser	His	Thr	Gln	Ser	Val	225	230	235	240
Thr	Ala	Val	Lys	Trp	Gly	Gly	Asp	Gly	Leu	Leu	Tyr	Ser	Ser	Ser	Gln	245	250	255	
Asp	Arg	Thr	Ile	Lys	Ala	Trp	Arg	Ala	Gln	Asp	Gly	Val	Leu	Cys	Arg	260	265	270	

Thr Leu Gln Gly His Ala His Trp Val Asn Thr Met Ala Leu Ser Thr
 275 280 285
 Asp Tyr Val Leu Arg Lys Gly Ala Phe Asn Pro Ala Asp Ala Ser Val
 290 295 300
 Asn Pro Gln Asp Met Ser Gly Ser Leu Glu Val Leu Lys Glu Lys Ala
 305 310 315 320
 Leu Lys Arg Ser Asn Glu Val Arg Gly Gln Gly Pro Glu Arg Leu Val
 325 330 335
 Ser Gly Ser Glu Asp Phe Thr Leu Phe Leu Trp Ala Pro Ala Glu Glu
 340 345 350
 Lys Lys Pro Leu Gln Arg Met Thr Gly His Gln Ala Leu Ile Asn Glu
 355 360 365
 Val Leu Phe Ser Pro Asp Thr Arg Ile Ile Ala Ser Ala Ser Phe Asp
 370 375 380
 Lys Ser Ile Lys Leu Trp Asp Gly Lys Thr Gly Lys Phe Leu Thr Ser
 385 390 395 400
 Leu Arg Gly His Val Ser Ala Val Tyr Gln Ile Ala Trp Ser Ala Asp
 405 410 415
 Ser Arg Leu Leu Val Ser Gly Ser Ser Asp Ser Thr Leu Lys Val Trp
 420 425 430
 Asp Ser Lys Thr Lys Lys Leu Leu Ile Asp Leu Pro Gly His Ala Asp
 435 440 445
 Glu Val Tyr Ser Val Asp Trp Ser Pro Asp Gly Gln Arg Val Ala Ser
 450 455 460
 Gly Gly Lys Asp Lys Cys Leu Arg Ile Trp Arg Lys
 465 470 475

<210> 8

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HA epitope

<400> 8

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala

1

5

<210> 9

<211> 149

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 9
 cggatccaaa aaatgtatcc ctatgacgtc cccgattatg cctaccctta cgatgtacct 60
 gactacgcgt atccgtacga cgttccggac tatgctcagg agacggacac ggagcaagag 120
 gccacgccac atacgataca ggcgcgcca 149

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 10
 taaacgaggc ggcctatcg tat 23

<210> 11
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> modified_base
 <222> (12)
 <223> i

<220>
 <221> modified_base
 <222> (21)
 <223> i

<220>
 <221> modified_base
 <222> (24)
 <223> i

<220>
 <221> modified_base
 <222> (27)
 <223> i

<400> 11
 cgcagaattc cnttygaygt nccngtngay at 32

<210> 12
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> modified_base
 <222> (15)
 <223> i

<220>
 <221> modified_base
 <222> (24)
 <223> i

<400> 12
 ggtgctcgag cytgnggytg rtanatdatr tc

32

<210> 13
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Conserved
 peptide

<400> 13
 Pro Phe Asp Val Pro Val Asp Ile
 1 5

<210> 14
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Conserved
 peptide

<400> 14
 Asp Ile Ile Tyr Gln Pro Gln
 1 5

<210> 15
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 15
caccagataa actgcagtta g

21

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
ctgtttcaac tgattgcttc t

21